

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2012; month=1; day=18; hr=13; min=34; sec=2; ms=40;]

=====

Application No: 08422548 Version No: 2.0

Input Set:

Output Set:

Started: 2012-01-12 15:02:57.842
Finished: 2012-01-12 15:02:59.086
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 244 ms
Total Warnings: 0
Total Errors: 0
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: HUMAN MPL LIGAND

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:08422548
(B) FILING DATE: 2012-01-12
(A) APPLICATION NUMBER:08422548
(B) FILING DATE: 2012-01-12
(C) CLASSIFICATION:435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08223263
(B) FILING DATE: 1994-04-04

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:US/08/223,263A
(B) FILING DATE: 04-Apr-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 3-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Daryl B.
(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: P0871P3

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415/225-1249
- (B) TELEFAX: 415/952-9881
- (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
-21 -20 -15 -10

Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
-5 1 5

Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
10 15 20

Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val
25					30						35			

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50

Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
55 60 65

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
70 75 80

Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
85 90 95

Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
100 105 110

Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
115 120 125

Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
120 125 130 135 140

Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Pro Thr Thr
145 150 155

Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
160 165 170

Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
 175 180 185

 Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
 190 195 200

 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
 205 210 215

 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
 220 225 230

 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
 235 240 245

 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
 250 255 260

 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
 265 270 275

 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
 280 285 290

 Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
 295 300 305

 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
 310 315 320

 Ser Gln Asn Leu Ser Gln Glu Gly
 325 330 332

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50

 CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100

 CCCCCACCCCTA CTCTGCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150

 CCCAGGAAGG ATTCAGGGGA GAGGCCCAA ACAGGGAGCC ACGCCAGCCA 200

 GACACCCCGG CCAGA ATG GAG CTG ACT GAA TTG CTC CTC 239
 Met Glu Leu Thr Glu Leu Leu Leu
 -21 -20 -15

GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 278
Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser
-10 -5

AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 317
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
1 5 10

AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 356
Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25

AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 395
Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
30 35

CTG CTG CCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 434
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
40 45 50

ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 473
Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly
55 60 65

GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG 512
Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
70 75

GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG 551
Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
80 85 90

CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG 590
Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
95 100

CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 629
Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
105 110 115

ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC 668
Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser
120 125 130

TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG 707
Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
135 140

CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA 746
Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro
145 150 155

CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC 785
Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu
160 165

ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG 824

Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu
170 175 180

GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT 863
Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
185 190 195

GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT 902
Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
200 205

CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA 941
Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln
210 215 220

ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT 980
Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
225 230

GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC 1019
Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr
235 240 245

CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA 1058
Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr
250 255 260

GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 1097
Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro
265 270

TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC 1136
Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe
275 280 285

CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC 1175
Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
290 295

CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC 1214
His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr
300 305 310

CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1253
Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser
315 320 325

CAG AAT CTG TCT CAG GAA GGG T AAGGT TCTCAGACAC 1290
Gln Asn Leu Ser Gln Glu Gly
330 332

TGCCGACATC AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC 1340

CCTGGGAGAC AACTGGACAA GATTCCTAC TTTCTCCTGA AACCCAAAGC 1390

CCTGGTAAAA GGGATACACA GGACTGAAA GGAAATCATT TTTCAGTGTA 1440

CATTATAAAC CTTCAGAAGC TATTTTTTA AGCTATCAGC AATACTCATC 1490
AGAGCAGCTA GCTCTTGTT CTATTTCTG CAGAAATTG CAACTCACTG 1540
ATTCTCTACA TGCTCTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG 1590
CCTGGCAGTT GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA 1640
AAGGGTAATT TCCTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC 1690
CCTTTACTAT CATTCTCACT GGGACTCTGA TCCCATATTC TTAACAGATC 1740
TTTACTCTG AGAAATGAAT AAGCTTCTC TCAGAAAAAA AAAAAAAAAA 1790
AAAAAA 1795

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
-16 -15 -10 -5

Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1 5 10

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25 26

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50

CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91
Leu Leu Leu Val Val Met Leu
-16 -15 -10

CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130
Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro
-5 1

CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169
Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg

5

10

15

GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210
Asp Ser His Val Leu His Ser Arg Leu
20 25 26

CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260

GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310

TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360

ACAGCCCCGA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTAGACCGAG AGCTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50

TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100

GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150

TTACCAAGTTA CGCGGATAAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200

GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250

CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300

AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350

ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp

35	40	45
Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala		
50	55	60
Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met		
65	70	75
Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu		
80	85	90
Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln		
95	100	105
Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala		
110	115	120
His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu		
125	130	135
Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu		
140	145	150
Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr		
155	160	165
Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly		
170	175	180
Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser		
185	190	195
Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly		
200	205	210
Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr		
215	220	225
Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe		
230	235	240
Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser		
245	250	255
Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly		
260	265	270
Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu		
275	280	285
Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His		
290	295	300
Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser		
305	310	315
Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln		

320

325

330

Glu Gly
332

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr
1				5				10				15		
Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala
	20				25							30		
Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys
		35				40						45		
Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala
		50				55						60		
Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu
		65			70							75		
Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro
		80				85						90		
Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu
		95				100						105		
Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser
		110				115						120		
Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala
		125				130						135		
Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg
		140			145							150		
Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp
		155			160							165		
Arg														
166														

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50

AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAAGGG GAGAGGCC 100

ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGA ATG GAG 143
Met Glu
-21 -20

CTG ACT GAT TTG CTC CTG GCG GCC ATG CTT CTT GCA GTG 182
Leu Thr Asp Leu Leu Ala Ala Met Leu Leu Ala Val
-15 -10

GCA AGA CTA ACT CTG TCC AGC CCC GTA GCT CCT GCC TGT 221
Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys
-5 1 5

GAC CCC AGA CTC CTA AAT AAA CTG CTG CGT GAC TCC CAC 260
Asp Pro Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His
10 15 20

CTC CTT CAC AGC CGA CTG AGT CAG TGT CCC GAC GTC GAC 299
Leu Leu His Ser Arg Leu Ser Gln Cys Pro Asp Val Asp
25 30

CCT TTG TCT ATC CCT GTT CTG CTG CCT GCT GTG GAC TTT 338
Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp Phe
35 40 45

AGC CTG GGA GAA TGG AAA ACC CAG ACG GAA CAG AGC AAG 377
Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys
50 55

GCA CAG GAC ATT CTA GGG GCA GTG TCC CTT CTA CTG GAG 416
Ala Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Glu
60 65 70

GGA GTG ATG GCA GCA CGA GGA CAG TTG GAA CCC TCC TGC 455
Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys
75 80 85

CTC TCA TCC CTC CTG GGA CAG CTT TCT GGG CAG GTT CGC 494
Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg
90 95

CTC CTC TTG GGG GCC CTG CAG GGC CTC CTA GGA ACC CAG 533
Leu Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln
100 105 110

GGC AGG ACC ACA GCT CAC AAG GAC CCC AAT GCC CTC TTC 572
Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe
115 120

TTG AGC TTG CAA CAA CTG CTT CGG GGA AAG GTG CGC TTC 611

Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe
125 130 135